EX18404（東京工業大学推薦課題）

飯田　慎仁（大阪大学蛋白質研究所）
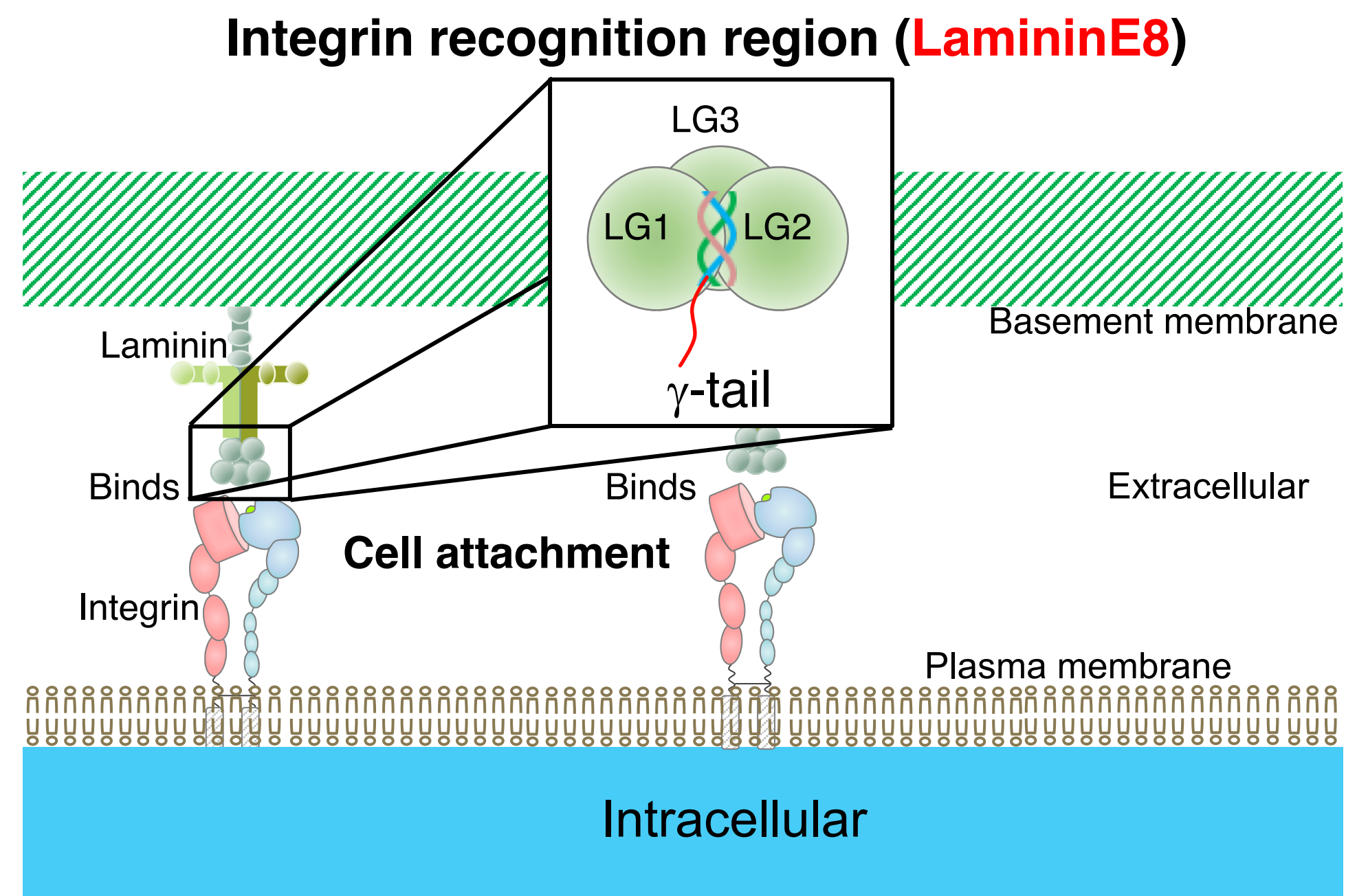
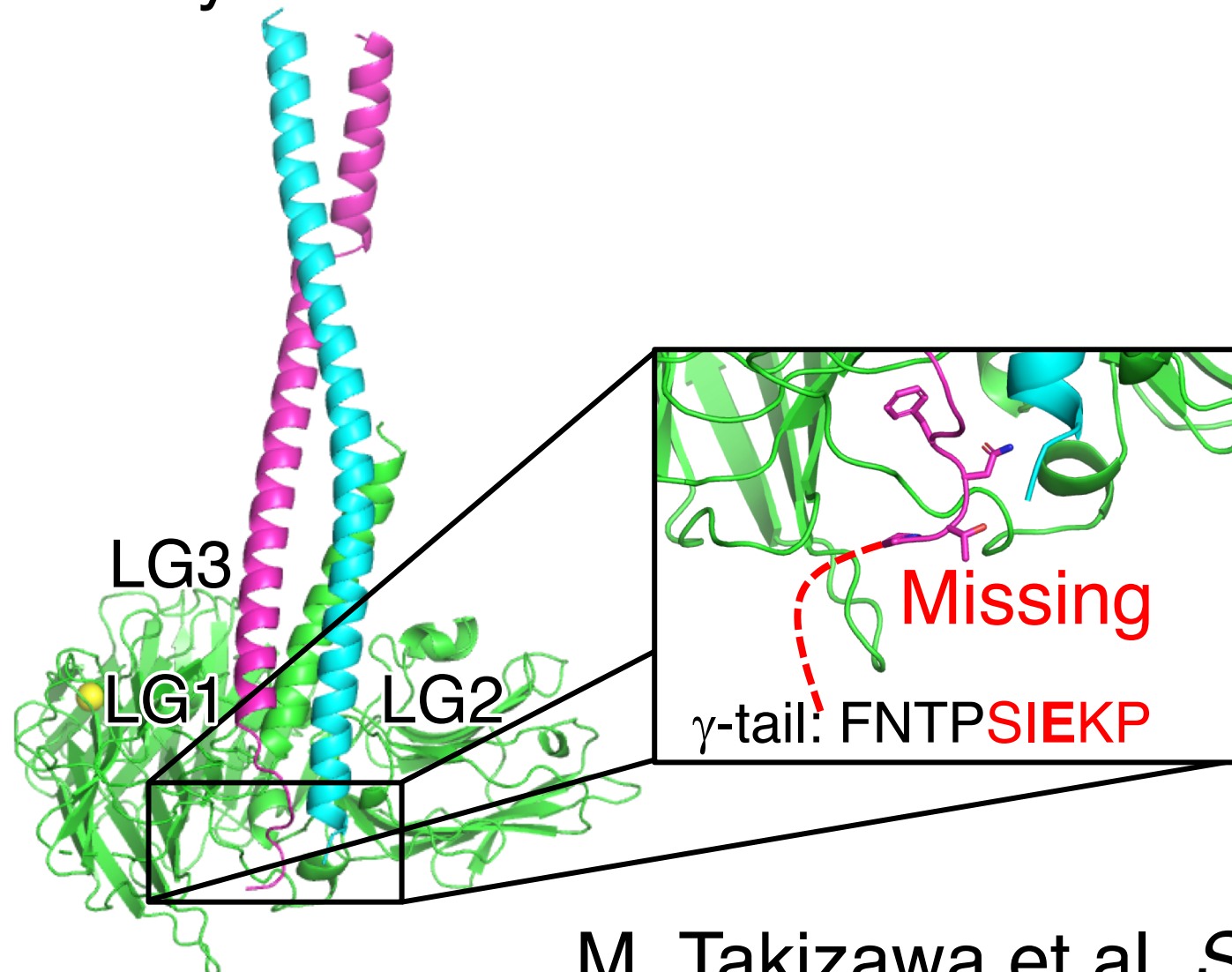## 全原子分子動力学法を用いた細胞外マトリックス蛋白質の相互作用解析

Background: Laminin is one of the basement proteins.
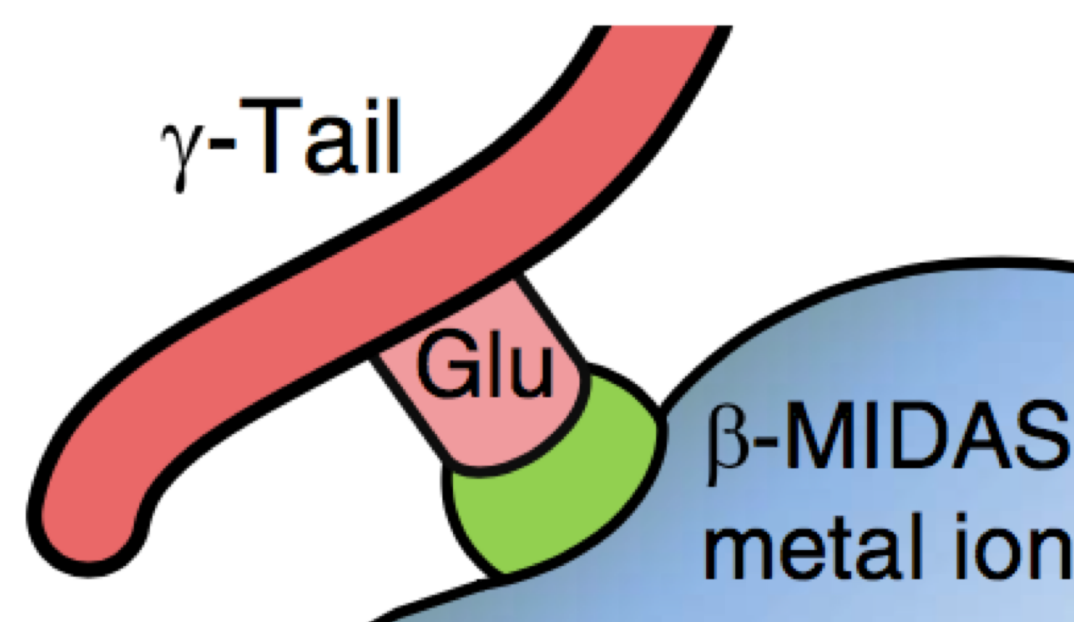
Basement membranes are ubiquitous

Integrin recognition region (LamininE8)
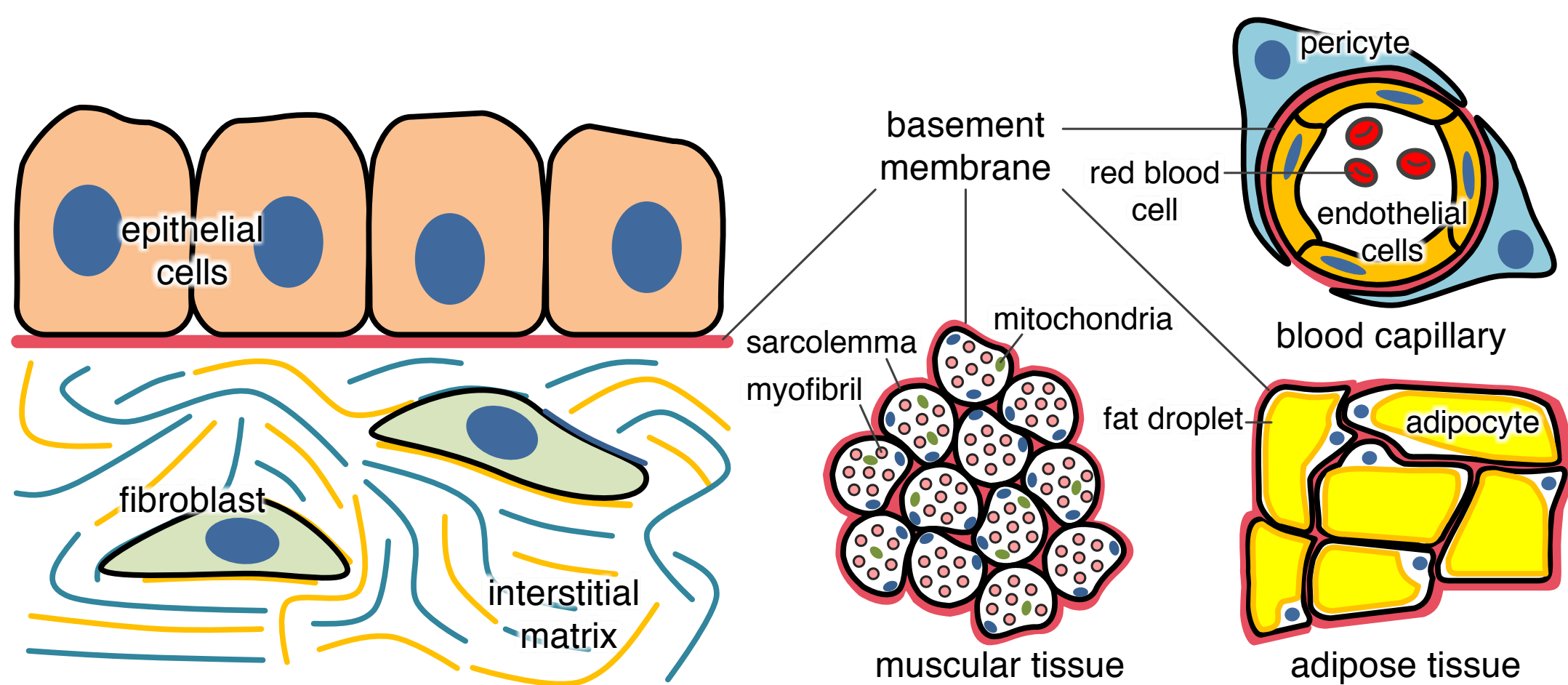
Question: How does the laminin E8 recognize an integrin?

Earlier Studies

X-ray structure: Laminin E8

LG3, LG1, LG2

Missing

γ-tail: FNTPSIEKP

The Glu1607 is positioned at a region in an integrin.

γ-Tail — Glu — β-MIDAS metal ion

By disulfide bond screening for the tail peptide and an integrin.
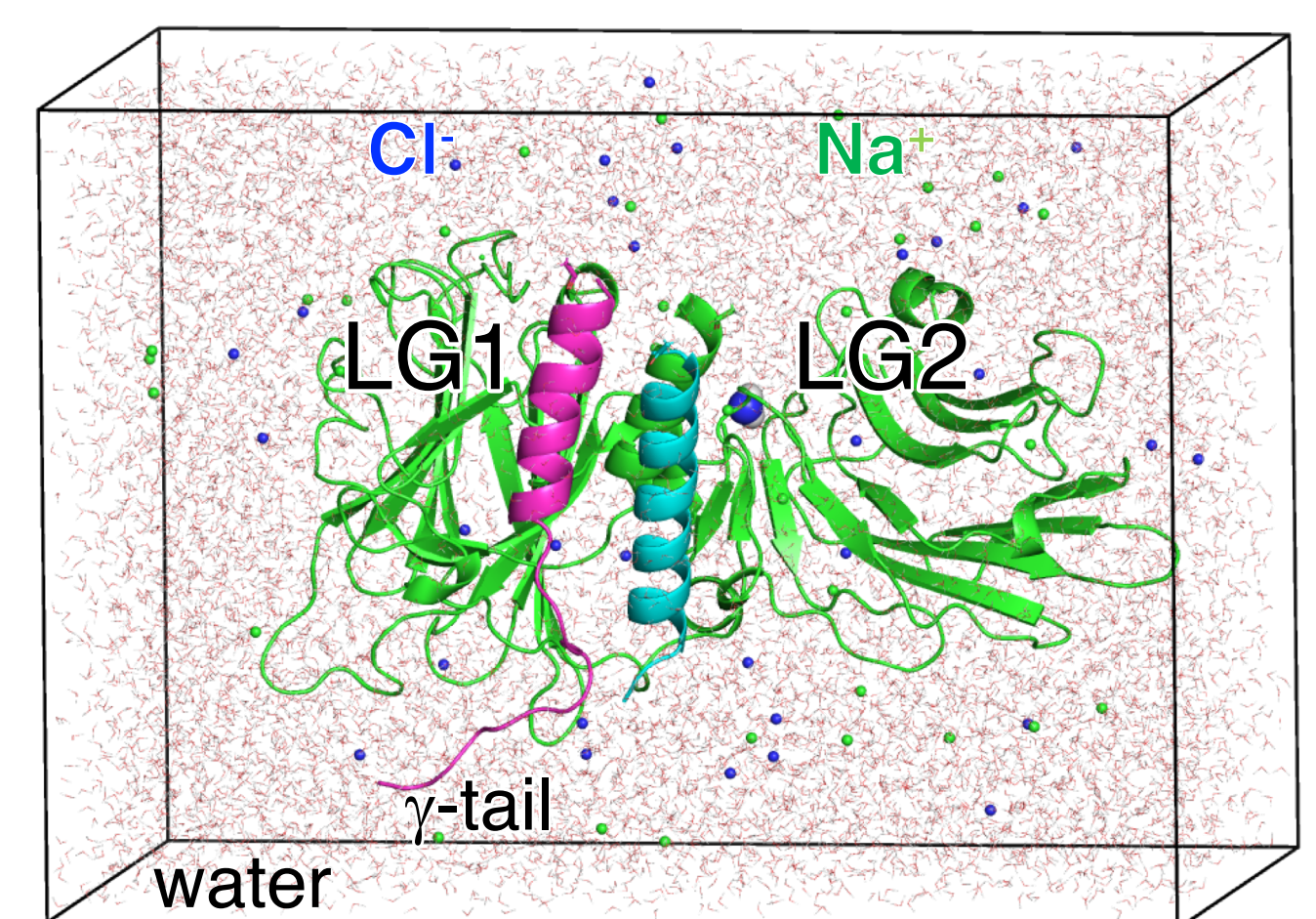
Hypothesis

Laminin E8 exposes Glu1607 to the binding site of the integrin ahead of time?

Integrin-binding activity could benefit from such structures.

M. Takizawa et al. *Sci. Adv.*, **2017**, *3*, e1701497.

Materials and Methods

I use **all-atom molecular dynamics (MD) simulation combined with a generalized ensemble (GE) method** in order to enhance structural sampling beyond that of conventional MD. The GE method is called virtual-system coupled Multicanonical Molecular Dynamics (V-McMD). I have already prepared a simulated system of laminin E8 (Right figure), which is being used in our simulations.

Future Plan

By performing V-McMD simulations, a variety of structures of laminin E8 will be obtained, and that hypothesis will be verified. Moreover, I will show that my computational results would predict unknown phenomena for interaction of laminin E8 with an integrin. The prediction will be confirmed by my collaborators who will perform experiments.